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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Staphylococcus aureus* 118 (ST772), a Major Disease Clone from India

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We report the draft genome sequence of an ST772 *Staphylococcus aureus* disease isolate carrying staphylococcal cassette chromosome *mec* (SCC*mec*) type V from a pyomyositis patient. Our *de novo* short read assembly is ~2.8 Mb and encodes a unique Panton-Valentine leukocidin (PVL) phage with structural genes similar to those of φ7247PVL and novel lysogenic genes at the N termini.

Community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) has become a major disease threat in the community as well as in hospitals (5, 8). Until 2004, hospital-associated MRSA, carrying the staphylococcal cassette chromosome *mec* (SCC*mec*) types III and IIIA, was common in India (2). Now, these are being replaced by CA-MRSA strains carrying SCC*mec* types IV (EMRSA-15) and V (ST772) in Indian hospitals (6, 9). These newer variants also carry several toxins and virulence factors, including Panton-Valentine leukocidin (PVL). ST772, called the Bengal Bay clone by some, was previously reported only in Bangladesh, India, and Malaysia but is now being reported in England, Ireland, and several other European countries (1, 4, 10).

We obtained genomic DNA from an *S. aureus* isolate belonging to ST772 (designated strain 118) from a pyomyositis patient (7), fragmented it to 300 to 400 bp, and sequenced these fragments on an Illumina HiSeq 1000 sequencer, thus obtaining ~53 million 75-mer reads (~26.5 million pairs). For further analysis, we selected reads based on the following three criteria: (i) average read quality of ≥35, (b) minimum base quality of ≥30, and (c) no undetermined base. This gave us ~6.4 million read pairs, with an overall coverage of ~350. Since coverage of >50× to 100× might compromise the quality of assemblies produced by the software Velvet (11), we randomly sampled ~15% of reads from these data and used them for the assembly process. The assembly was performed on three sets of independently sampled read sets to ensure consistency. In addition, we also performed a similar sequencing of *S. aureus* USA300, for which a reference genome sequence is already available.

The draft assembly of the genome of *S. aureus* 118 (ST772) covers ~2.81 million base pairs. These bases are covered by 67, 72, and 73 contigs in the three assemblies attempted. Paired-end mapping of all raw reads to the contigs predicts an insert size distribution which is similar to that obtained by mapping our USA300 reads to its fully sequenced reference sequence. Finally, ~94 to 95% of the bases in our contigs fall within alignments to fully sequenced *S. aureus* genomes (BLASTN; E value $< 10^{-100}$).

We identified 2,524 protein-coding genes predicted by Glimmer in two of the three assemblies constructed here. Of these, 2,459 (97%) have a counterpart with significant similarity (phmmer, http://hmmer.janelia.org; E value $< 10^{-10}$; ≥40% global sequence identity) in at least one fully sequenced *S. aureus* genome. We also detected an ~42-kb PVL phage sequence by using signature sequences published earlier (3). Comparison of this sequence with five other sequenced PVL phages (φPVL, φ108PVL, φSLT, φSa2958, and φ7247PVL) showed that it is closest to the φ7247PVL phage from *S. aureus* ST59 (12). However, the best-aligning regions are largely restricted to the structural regions, with considerable variations in the lysogeny region.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at GenBank under the accession number AJGE00000000. The version described in this paper is the first version. The raw Illumina sequencing reads have been deposited with the Short Read Archive and are available under the accession number SRX118450.

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